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DOCUMENT NUMBER: 141:152251

TITLE: Genetic polymorphisms in genes and their transcripts and encoded proteins associated with myocardial infarction and their uses in diagnosis and drug screening

INVENTOR(S): Cargill, Michele; Devlin, James J.; Iakoubova, Olga

PATENT ASSIGNEE(S): Applera Corporation, USA

SOURCE: PCT Int. Appl., 145 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 16

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004058052	A2	20040715	WO 2003-XM340978	20031222
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2004058052	A2	20040715	WO 2003-US340978	20031222
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
PRIORITY APPLN. INFO.:				
			US 2002-434778P	P 20021220
			US 2003-453135P	P 20030310
			US 2003-466412P	P 20030430
			US 2003-504955P	P 20030923
			WO 2003-US40978	A 20031222

AB The present invention is based on the discovery of genetic polymorphisms that are associated with myocardial infarction. In particular, the present invention relates to nucleic acid mols. containing the polymorphisms, variant proteins encoded by such nucleic acid mols., reagents for detecting the polymorphic nucleic acid mols. and proteins, and methods of using the nucleic acid and proteins as well as methods of using reagents for their detection. [This abstract record is one of 15 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.]

ACCESSION NUMBER: 2002:350748 CAPLUS

DOCUMENT NUMBER: 136:336018

TITLE: The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome

AUTHOR(S): Camargo, Anamaria A.; Samaia, Helena P. B.; Dias-Neto, Emmanuel; Simao, Daniel F.; Migotto, Italo A.; Briones, Marcelo R. S.; Costa, Fernando F.; Nagai, Maria Aparecida; Verjovski-Almeida, Sergio; Zago, Marco A.; Andrade, Luis Eduardo C.; Carrer, Helaine; El-Dorry, Hamza F. A.; Espreafico, Enilza M.; Habr-Gama, Angelita; Giannella-Neto, Daniel; Goldman, Gustavo H.; Gruber, Arthur; Hackel, Christine; Kimura,

Edna T.; Maciel, Rui M. B.; Marie, Suely K. N.;  
 Martins, Elizabeth A. L.; Nobrega, Marina P.;  
 Paco-Larson, Maria Luisa; Pardini, Maria Ines M. C.;  
 Pereira, Goncalo G.; Pesquero, Joao Bosco; Rodrigues,  
 Vanderlei; Rogatto, Silvia R.; Da Silva, Ismael D. C.  
 G.; Sogayar, Mari C.; Sonati, Maria De Fatima; Tajara,  
 Eloiza H.; Valentini, Sandro R.; Alberto, Fernando L.;  
 Amaral, Maria Elisabete J.; Aneas, Ivy; Arnaldi,  
 Liliane A. T.; De Assis, Angela M.; Bengtson, Mario  
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 Carraro, Dirce M.; Cerutti, Janete M.; Correa, Maria  
 Lucia C.; Correa, Rosana F. R.; Costa, Maria Cristina  
 R.; Curcio, Cyntia; Hokama, Paula O. M.; Ferreira, Ari  
 J. S.; Furuzawa, Gilberto K.; Gushiken, Tsieko; Ho,  
 Paulo L.; Kimura, Elza; Krieger, Jose E.; Leite,  
 Luciana C. C.; Majumder, Paromita; Marins, Mozart;  
 Marques, Everaldo R.; Melo, Analy S. A.; Barbosa de  
 Melo, Monica; Mestriner, Carlos Alberto; Miracca,  
 Elisabete C.; Miranda, Daniela C.; Nascimento, Ana  
 Lucia T. O.; Nobrega, Francisco G.; Ojopi, Elida P.  
 B.; Pandolfi, Jose Rodrigo C.; Pessoa, Luciana G.;  
 Prevedel, Aline C.; Rahal, Paula; Rainho, Claudia A.;  
 Reis, Eduardo M. R.; Ribeiro, Marcelo L.; Da Ros,  
 Nancy; De Sa, Renata G.; Sales, Magaly M.; Sant'anna,  
 Simone Cristina; Dos Santos, Mariana L.; Da Silva,  
 Aline M.; Da Silva, Neusa P.; Silva, Wilson A., Jr.;  
 Da Silveira, Rosana A.; Sousa, Josane F.; Stecconi,  
 Daniella; Tsukumo, Fernando; Valente, Valeria; Soares,  
 Fernando; Moreira, Eloisa S.; Nunes, Diana N.; Correa,  
 Ricardo G.; Zalberg, Heloisa; Carvalho, Alex F.;  
 Reis, Luis F. L.; Brentani, Ricardo R.; Simpson,  
 Andrew J. G.; De Souza, Sandro J.

CORPORATE SOURCE:

Ludwig Institute for Cancer Research, Sao Paulo,  
 01509-010, Brazil

SOURCE:

Proceedings of the National Academy of Sciences of the  
 United States of America (2001), 98(21), 12103-12108  
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AB Open reading frame expressed sequences tags (ORESTES) differ from  
 conventional ESTs by providing sequence data from the central protein  
 coding portion of transcripts. A total of 696,745 ORESTES sequences were  
 generated from 24 human tissues and a subset of the data that correspond  
 to a set of 15,095 full-length mRNAs used as a means of assessing the  
 efficiency of the strategy and its potential contribution to the  
 definition of the human transcriptome. It was estimated that ORESTES sampled  
 over 80% of all highly and moderately expressed, and between 40% and 50%  
 of rarely expressed, human genes. In the most thoroughly sequenced  
 tissue, the breast, the 130,000 ORESTES generated are derived from  
 transcripts from an estimated 70% of all genes expressed in that tissue, with  
 an equally efficient representation of both highly and poorly expressed  
 genes. In this respect, the capacity of the ORESTES strategy both for  
 gene discovery and shotgun transcript sequence generation significantly  
 exceeds that of conventional ESTs. The distribution of ORESTES is such  
 that many human transcripts are now represented by a scaffold of partial  
 sequences distributed along the length of each gene product. The exptl.  
 joining of the scaffold components, by reverse transcription-PCR,  
 represents a direct route to transcript finishing that may represent a  
 useful alternative to full-length cDNA cloning. [This abstract record is  
 one of 186 records for this document necessitated by the large number of  
 index entries required to fully index the document and publication system  
 constraints.]

L19 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2002:778221 CAPLUS

DOCUMENT NUMBER: 137:288988

TITLE: Antisense modulation of urokinase plasminogen

activator expression for treatment of cancer  
Baker, Brenda F.; Freier, Susan M.; Watt, Andrew T.  
Isis Pharmaceuticals, Inc., USA  
PCT Int. Appl., 153 pp.  
CODEN: PIXXD2

INVENTOR(S):  
PATENT ASSIGNEE(S):  
SOURCE:  
DOCUMENT TYPE:  
LANGUAGE:  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002079515	A1	20021010	WO 2002-US8112	20020318
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004043957	A1	20040304	US 2003-665216	20030919

PRIORITY APPLN. INFO.:  
US 2001-821972 A 20010330  
AB Antisense compds., compns. and methods are provided for modulating the expression of urokinase plasminogen activator. The composition comprise antisense compds., particularly antisense oligonucleotides, targeted to nucleic acids encoding urokinase plasminogen activator. Method of using these compds. for modulation of urokinase plasminogen activator expression and for treatment of diseases associated with expression of urokinase plasminogen activator are provided.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT